



UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/776,213	02/12/2004	Graham P. Belfield	3764-152	2071

23117 7590 03/10/2005

NIXON & VANDERHYE, PC
1100 N GLEBE ROAD
8TH FLOOR
ARLINGTON, VA 22201-4714

EXAMINER

LEFFERS JR, GERALD G

ART UNIT	PAPER NUMBER
----------	--------------

1636

DATE MAILED: 03/10/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

10/776,213

Applicant(s)

BELFIELD ET AL.

Examiner

Gerald G. Leffers Jr., PhD

Art Unit

1636

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 17 December 2004.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-29 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-9, 11-18, 20 and 22-29 is/are rejected.
- 7) ☒ Claim(s) 10, 19 and 21 is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☒ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 12 February 2004 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☒ All b) ☐ Some * c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
 - ☒ Certified copies of the priority documents have been received in Application No. 09/743,194
 - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date 2/12/2004.

- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☒ Other: Exhibit A, SEARCH RESULT SEQ ID NO: 2

DETAILED ACTION***Election/Restrictions***

Applicant's election of Group II (claims 1-29 directed to SEQ ID NO: 2) in the reply filed on 12/17/2004 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

Information Disclosure Statement

Receipt is acknowledged of an information disclosure statement (IDS) filed on 2/12/2004. The signed and initialed PTO Form 1449 has been mailed with this action. The four search results (e.g. "B-Door External...") have not been considered as they were not present in the patent file. It is further noted that in any case there is no indication of the publication date for these references or where the information is available to the public (i.e. the publisher). If applicants want the information therein to be considered, the information should be resubmitted in a form consistent with 37 CFR 1.98.

Specification

The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed.

The following title is suggested: Compositions and Methods Using the Yeast HOR7 Promoter.

Art Unit: 1636

The disclosure is objected to because of the following informalities: at several places in the specification there are odd placements of letters and symbols at the beginning and ending of words. For example, on page 2 at lines 5 & 6, the term "Ayeast promoter@" is used. It appears as though the characters "A" and "@" are meant to be quotation marks around the word "yeast". Another example occurs at page 25, line 14. Numerous instances of these typographical errors are present throughout the specification. It would be remedial to amend the specification in each instance to clearly indicate that what is intended.

Claim Objections

Claims 10 & 21 are objected to because of the following informalities: each recites nonelected inventions (i.e. the different vector constructs comprising the nonelected promoter elements). It would be remedial to amend the claims to be directed to the two elected embodiments (i.e. pYMR251AP + luc and pYMR251AP). Appropriate correction is required.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1-6 are rejected under 35 U.S.C. 101 because the claims read on nonstatutory subject matter. The claims are directed to "A yeast promoter which comprises at least [17, 50, 100, 200, 300 or 400] contiguous nucleotides of an isolated and purified polynucleotide which is SEQ ID NO: 2..." without any explicit limitation as to what context the promoter is found. The terms "isolated and purified polynucleotide" refer to SEQ ID NO:2 and not to the promoter that

Art Unit: 1636

is claimed. As written, the claim can be interpreted to encompass any promoter that meets the limitation of comprising at least 17 contiguous nucleotides of SEQ ID NO: 2, regardless of the context in which the promoter is found. By this interpretation, the rejected claims read on the native YMR251WA promoter.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-6 are rejected under 35 U.S.C. 102(b) as being anticipated by Hunt et al (see the attached search report for Accession No. Z48639) as evidenced by Goffeau et al (Science, 1996, Vol. 274, pages 546-567; see the entire reference).

Accession No. 48639 corresponds to *S. cerevisiae* cosmid clone 9920, which has 99.6 identity with SEQ ID NO: 2 over its entire length. The sequence of clone 9920 was submitted by Hunt et al as early as 10 March 1995 and was apparently available to the public as of 11 August 1997. Goffeau et al teach that the entire *S. cerevisiae* genomic sequence was known by October 1996.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

Art Unit: 1636

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-6, 8-9, 11-18, 20, 22-28 rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to a yeast promoter, vectors and host cells comprising the promoter. Some of the rejected claims are directed to methods of expressing a protein featuring the promoter, where the promoter comprises at least 17 contiguous nucleotides of SEQ ID NO: 2 and wherein the promoter can drive expression of a nucleic acid molecule encoding the polypeptide when operatively linked thereto. The promoter can be operative in any cell type (e.g. claims 1-6) or must at least be operative in yeast (e.g. claim 8). The promoter may have at least 50, 100, 200, 300, 400 contiguous nucleotides of SEQ ID NO: 2. Alternatively, the promoter can comprise the entire 723 nucleotides of SEQ ID NO: 2. For many of the claims, the level of promoter activity is controlled by the level of fermentable carbon source (e.g. glucose) and/or non-fermentable carbon source (e.g. ethanol) in the culture medium.

SEQ ID NO: 2 describes a 723 nucleotide sequence. Even for embodiments featuring a promoter comprising as much as 400 contiguous nucleotides of SEQ ID NO: 2, there are a very large number of possible fragments of SEQ ID NO: 2 that may or may not retain promoter activity. As the number of contiguous nucleotides of SEQ ID NO: 2 that must be present in the claimed promoter or promoter fragment decreases, the number of possible fragments that must

Art Unit: 1636

function as a promoter greatly increases (e.g. 17 contiguous nucleotides out of 723). Thus, the claims are broad genus claims encompassing a large number of fragments of SEQ ID NO: 2 that must retain functional activity as a promoter element. The size of the genus is further compounded by the functional limitation in at least some of the claims that the promoter must be responsive to fermentable and non-fermentable carbon sources in culture media.

SEQ ID NO: 2 is 723 nucleotides in length and describes a sequence that is found at the beginning of the 7MR251WA (HOR7) reading frame (e.g. see Figure 14 of the instant specification). The specification describes the cloning of SEQ ID NO: 2 into an expression vector with an operatively linked reporter polypeptide (i.e. encoding luciferase) to demonstrate that the sequence described by SEQ ID NO: 2 has promoter activity and that the activity is responsive to both glucose and ethanol in culture media (e.g. Table 7). No description is provided, however, for any fragment of SEQ ID NO: 2 of any length that retains promoter activity. No description is provided in the instant specification for any sequence within SEQ ID NO: 2 that resembles any known transcription factor binding sequence (e.g. GAL4, etc.). The specification provides no guidance with regard to which fragments within SEQ ID NO: 2 might be essential for response to fermentable or non-fermentable carbon sources in culture media.

The prior art does not offset the deficiencies of the instant specification with regard to description of the claimed invention. Promoter sequences comprising SEQ ID NO: 2 do not appear to have been described in the prior art. While one of skill in the art might be able to identify sequences within SEQ ID NO: 2 that possess some homology to binding sites for known transcription factors, there may be other unknown transcription factors required for even the basal level of promoter activity associated with SEQ ID NO: 2, much less glucose- or ethanol-

Art Unit: 1636

responsive activities. Again, there is no description in the art of record for regulatory sequences that control expression of HOR7 in yeast.

Given the great number of possible fragments of SEQ ID NO: 2 encompassed by the rejected claims and the limitation that the fragments must retain at least some functional activity, and given the lack of a structural/functional basis in the instant specification or prior art for the skilled artisan to envision those embodiments that actually do retain promoter activity, the skilled artisan would not have been able to envision a sufficient number of the claimed embodiments to describe the broadly claimed genus. Therefore, the skilled artisan would have reasonably concluded applicants were not in possession of the claimed invention.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter that the applicant regards as his invention.

Claim 7 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 7 is vague and indefinite in that the metes and bounds of the phrase "which is SEQ ID NO: 2" are unclear. As written, the phrase can be applied to the "yeast promoter" itself, or alternatively, to the isolated and purified polynucleotide. It is thus unclear whether the claim is limited to SEQ ID NO: 2 or can encompass a promoter comprising sequences in addition to SEQ ID NO: 2.

Art Unit: 1636

Conclusion

Claims 1-9, 11-18, 20 & 22-28 are rejected. Claims 10, 19 & 21 are objected to as being directed to nonelected embodiments. Claim 29 is allowable.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Gerald G. Leffers Jr., PhD whose telephone number is (571) 272-0772. The examiner can normally be reached on 6:30-4:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Remy Yucel can be reached on (571) 272-0781. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).


GERRY LEFFERS
PRIMARY EXAMINER

Gerald G Leffers Jr., PhD
Primary Examiner
Art Unit 1636

ggl

```

Db      136 GGGGCTAAGAGTCAATCACTTTCTTTCCCTTCGGCTCGGACCGGGACCCCTCCT 195
Qy      181 CTCGCCGACCATTTCTTCCCTTCATATCTTCCCTTTATTCCTATCCGCTTGAAGCAACC 240
Db      196 CTCGCCGACCATTTCTTCCCTTCATATCTTCCCTTTATTCCTATCCGCTTGAAGCAACC 255
Qy      241 GCATATGACTAAATGGTGTGGACATCTCCATGGCTGTGACTGTGTGTATCTCACAGT 300
Db      256 GCATATGACTAAATGGTGTGGACATCTCCATGGCTGTGACTGTGTGTATCTCACAGT 315
Qy      301 GGTAAAGCGCAGTGGCTCGGAACCGTTCCTTGTGTGACAAATCTAGAACAGGGGCTTACA 360
Db      316 GGTAAAGCGCAGTGGCTCGGAACCGTTCCTTGTGTGACAAATCTAGAACAGGGGCTTACA 375
Qy      361 GTCTCGATAATAGATAATAAGCGCATTTTGTAGCGCGCGCGCGCGCGCGCTTCCCA 420
Db      376 GTCTCGATAATAGATAATAAGCGCATTTTGTAGCGCGCGCGCGCGCGCGCTTCCCA 435
Qy      421 ATAGGAGCGCGAGTTTATCGCGCGAGCTCTACTTTCTTCTTATTTGGTAAAGCCCTTTC 480
Db      436 ATAGGAGCGCGAGTTTATCGCGCGAGCTCTACTTTCTTCTTATTTGGTAAAGCCCTTTC 495
Qy      481 TGTTCGCGCAGTGGTGTGCGAGCTGCGCGGAGCAACATAGTATAGGGATGTAAAC 540
Db      496 TGTTCGCGCAGTGGTGTGCGAGCTGCGCGGAGCAACATAGTATAGGGATGTAAAC 555
Qy      541 TTTGATGAGAGATTAGCAAGCGGAAATTTGTCTACTATGTGACAGTTTCTGGGAGCTTAACTTT 600
Db      556 TTTGATGAGAGATTAGCAAGCGGAAATTTGTCTACTATGTGACAGTTTCTGGGAGCTTAACTTT 615
Qy      601 TCATATAAAGGGAGAAATTTGTCTACTATGTGACAGTTTCTGGGAGCTTAACTTT 660
Db      616 TCATATAAAGGGAGAAATTTGTCTACTATGTGACAGTTTCTGGGAGCTTAACTTT 675
Qy      661 TATTGACAGGACTATCAATCATACAGATATGTCAAAAAAAGAGATAATAATAA 720
Db      676 TATTGACAGGACTATCAATCATACAGATATGTCAAAAAAAGAGATAATAATAA 735
Qy      721 CAT 723
Db      736 CAT 738

RESULT 4
AR492055
LOCUS      AR492055      850 bp      DNA      linear      PAT 15-MAY-2004
DEFINITION Sequence 30 from patent US 6716601.
ACCESSION AR492055
VERSION    AR492055.1 GI:47260524
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 850)
AUTHORS     Belfield,G.P. and Oakley,C.
TITLE       Compositions and methods utilizing the yeast 2B01 promoter
JOURNAL     Patent: US 6716601-A 30 06-APR-2004;
FEATURES    Location/Qualifiers
             source
               1..850
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Query Match      99.6%; Score 720.4; DB 6; Length 850;
Best Local Similarity 99.9%; Pred. No. 2.4e-206;
Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CTTTCGATTAGCACGCACACATCACATGACTGGTCAATAAATAATACATTACGGAATA 60
Db      78 CTTTCGATTAGCACGCACACATCACATGACTGGTCAATAAATAATACATTACGGAATA 137
Qy      61 ACCATAAGAGCAAGCGGATCTACTTGTGAAGGAAAGGAGCACGCTGTGAAGGGGAT 120

```

```

Db      138 ACCATAAGAGCAAGCGATACCTACTTGGAGGAAAAAGGAGCAGCGTTGTAGGGGGAT 197
Qy      121 GGGGGCTAAGAGTCAATCACTTTCTTTCCCTTCGGGTCCGACCCGGGACCCCTCCT 180
Db      198 GGGGGCTAAGAGTCAATCACTTTCTTTCCCTTCGGGTCCGACCCGGGACCCCTCCT 257
Qy      181 CTCGCCGACCATTTCTTCCCTTCATATCTTCTTTTATTCCTATCCGTTGAAGCAACC 240
Db      258 CTCGCCGACCATTTCTTCCCTTCATATCTTCTTTTATTCCTATCCGTTGAAGCAACC 317
Qy      241 GCATATGACTAAATGGTGTGGACATCTCCATGGCTGTGACTGTGTGTATCTCACAGT 300
Db      318 GCATATGACTAAATGGTGTGGACATCTCCATGGCTGTGACTGTGTGTATCTCACAGT 377
Qy      301 GGTAAAGCGCAGTGGCTCGGAACCGTTCCTTGTGTGACAAATCTAGAACAGGGGCTTACA 360
Db      378 GGTAAAGCGCAGTGGCTCGGAACCGTTCCTTGTGTGACAAATCTAGAACAGGGGCTTACA 437
Qy      361 GTCTCGATAATAGATAATAAGCGCATTTTGTAGCGCGCGCGCGCGCGCTTCCCA 420
Db      438 GTCTCGATAATAGATAATAAGCGCATTTTGTAGCGCGCGCGCGCGCGCTTCCCA 497
Qy      421 ATAGGAGCGCGAGTTTATCGCGGAGCTCTACTTTCTTCTTATTTGGTAAAGCCCTTTC 480
Db      498 ATAGGAGCGCGAGTTTATCGCGGAGCTCTACTTTCTTCTTATTTGGTAAAGCCCTTTC 557
Qy      481 TGTTCGCGCAGTGGTGTGCGAGCTGCGCGGAGCAACATAGTATAGGGATGTAAAC 540
Db      558 TGTTCGCGCAGTGGTGTGCGAGCTGCGCGGAGCAACATAGTATAGGGATGTAAAC 617
Qy      541 TTTGATGAGAGATTAGCAAGCGGAAATTTGTCTACTATGTGACAGTTTCTGGGAGCTTAACTTT 600
Db      518 TTTGATGAGAGATTAGCAAGCGGAAATTTGTCTACTATGTGACAGTTTCTGGGAGCTTAACTTT 677
Qy      601 TCATATAAAGGGAGAAATTTGTCTACTATGTGACAGTTTCTGGGAGCTTAACTTT 660
Db      678 TCATATAAAGGGAGAAATTTGTCTACTATGTGACAGTTTCTGGGAGCTTAACTTT 737
Qy      661 TATTGACAGGACTATCAATCATACAGATATGTCAAAAAAAGAGATAATAATAA 720
Db      738 TATTGACAGGACTATCAATCATACAGATATGTCAAAAAAAGAGATAATAATAA 797
Qy      721 CA 722
Db      798 AA 799

RESULT 5
SC9920
LOCUS      S.cerevisiae chromosome XIII comid 9920.
DEFINITION S.cerevisiae chromosome XIII comid 9920.
ACCESSION Z48639.1 GI:732924
VERSION    Z48639.1
KEYWORDS   COX7; cytochrome oxidase; delta element; glutamate decarboxylase;
            PET11; transfer RNA-Ala.
SOURCE      Saccharomyces cerevisiae (baker's yeast)
ORGANISM    Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1 (bases 1 to 23498)
AUTHORS     Hunt,S. and Bowman,S.
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 23498)
AUTHORS     Barrell,B., Rajandream,M.A. and Walsh,S.V.
JOURNAL     Direct Submission
TITLE       Submitted (10-MAR-1995) Saccharomyces cerevisiae chromosome XIII
            sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridge
            CB10 1RQ E-mail: barrell@sanger.ac.uk
COMMENT     Notes:
            All CDS over 100 codons have been analysed. CDS that are completely
            overlapped and those that are overlapped by more than 50%
            of their length by a larger CDS have been omitted from this
            analysis.

```

10/776,213
Exh. b. 1A
Applicant Copy

Details of the omitted CDS are available on request. The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons and the calculated codon adaptation index (CAI) is given for each CDS.

Cosmid 9920 is overlapped at the start of this sequence by cosmid 9408 and at the end of this sequence by cosmid 8156.

FEATURES

```

source      Location/Qualifiers
1..23498
/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/strain="AB972"
/db_xref="taxon:4932"
/chromosome="XIII"
/map="13K"
/clone="cosmid 9920"
complement (<1..2870)
PS00061 Short-chain alcohol dehydrogenase family
signature
/codon_start=1
/product="unknown"
/protein_id="CAA88574.1"
/db_xref="GI:732925"
/db_xref="UniProt/Swiss-Prot:Q04781"
/translation="MSFGINTQYNTDGLGNGVRSISLNFGLPDPPLNSLSLYS
NELKILFQSLRRDTTEKALMDLSNLSIDPQNEFYFNDIFLLCWSQIYAKLIISD
YKVIHQSLQITMLVSKLRKIKSLKDFPLILLGTCELDYSKPSLNELETCFN
KDPKALNAWFOQLNLNKEIVVNEEDTISDERYSKEESFRVHRVIAAGVLL
LIKLVHKNVQSSERNSSLSKVLTSDESILKLNKNGONTWATVTLRLDVLVTRGY
MPSHKNIKMLAKSLKSLTHITSKNIKLVCPVLSILNLLATLDVDEGTINWDKX
SKEKVLKLSVRSSTSPSGFNAPVALYSYKHSFLDYLEWLPFWQKSVQRLEKNG
FSARNSAVLNEFWNLKFAEDSEERVKGVSEIYFNSLSCGSLSEYTKLNQTLIS
GVFPDPKWEREDYTDSEDIRKIVSEKFNLFALLTSPNSESIRLDFDFVQLI
ETDPNSVKNYGDVADNLYFLDSMDIFLNGKIGFNEIPTLVQESTYQNFAGIMAQ
YSNKFQKNTDAITSLDFPVALSFNPKTIILATNWLNDIYQOLMKSDSLELE
LYIEDFMKNYKFDGSGEIPKGNKFLNQRTITTLVRSVANGVQEQFCALVSKLDET
FSTLLNTDLSLCALVESEDSNEKLFKLSLOLAKNSEIANKLAQVILQAOYFSP
GAKKYVTHAVELINGNDTSQIFPPANAIEVARYMPAIDYRSLSSLSLTHLL
TDDKINLNMOKLRIYALFDLADLALPVRNHIYVAFITVSELVDYDNCLEENP
DIYDFGHTFFHGKGNLNFSDIVGNVTPANGDAMLTFTDAESNSVYFFYSRVLY
KVLNLSIDTSSITNGLLASVESFVTXTRDQKSTDKYLL"
complement (2406..2438)
/note="PS00061 Short-chain alcohol dehydrogenase family
signature"
misc_feature
complement (3200..3272)
/product="tRNA-Ala"
/note="tRNA-Ala, anticodon agc, len: 73"
LTR
complement (3379..3706)
/note="delta element"
CDS
complement (join(4101..4196,4691..4780))
/note="YM9920.02c, unknown, len: 61, CAI: 0.17, possible
small spliced gene"
/codon_start=1
/product="unknown"
/protein_id="CAA88575.1"
/db_xref="GI:732926"
/db_xref="UniProt/TremBL:Q8X120"
/translation="MGEIAPMKNPDEGTINMCQSLRYQIMRMSIGLRRLLPLNNKAI
IPLNSLAHLCAIYTE"
complement (join(4101..4196,4434..4505))
/note="YM9920.03c, unknown, len: 55, CAI: 0.13, possible
small spliced gene"
/codon_start=1
/product="unknown"
/protein_id="CAA88576.1"
/db_xref="GI:732927"
/db_xref="UniProt/TremBL:Q8X1Y9"
/translation="MELVASCPRMPRYRHANDTLGWLIGLRLPLNNKAIIPNSL
ALAHLCALYTE"
misc_feature
complement (4197..4199)
/note="possible splice acceptor sequence, cag"

```

misc_feature
misc_feature
misc_feature
misc_feature
CDS

```

complement (4222..4228)
/note="possible splice branch sequence, tactaac"
complement (4428..4433)
/note="possible donor sequence, gtatgt"
complement (4685..4690)
/note="possible donor sequence, gtacgt"
complement (4689..4694)
/note="possible donor sequence, gtacgt"
5632..7389
/note="YM9920.04, unknown, len: 585, CAI: 0.18, putative
glutamate decarboxylase gene"
/codon_start=1
/product="unknown"
/protein_id="CAA88577.1"
/db_xref="GI:732928"
/db_xref="GOA:Q04792"
/db_xref="SGD:S0004862"
/db_xref="UniProt/Swiss-Prot:Q04792"
/translation="MLRRHSGKOKFNENIAGKVVDHLAGLLSLNDVQKSAVQSGHQG
SNNRDTSQGMANKYSPVKKGLPADLSYQIHNELTDGNPHNLNLASFNVTFTDQA
RKLIDENLTNLADNDEYQQLIELTORCISMLAQMLHANPDEEPIGCAITGSSAIML
GGLAMKRWHRMKNAGDASKPNIIMSSACVALEKFTFYFEVECLVPVSHRSHM
LDPESLWYVDENTIGCFVILGTTTGTGHLENKVDVLSQIEAKHPDWSNTHPIHA
DGASGGPILIPGEKEKHMKAYGMERGMFNHPRVVSMTSGHKFGLTTPGLGWLWRDE
SLADELRFKLXILGVEETFGLNFRPGFQVHVYFNVSLGHSGRTRFQNSLFLVA
RAFSFELLNSKLPGCCPEIYSSIHESIENDSAPKSKDYWEHPQAYKPGVLPVAFKLS
KATHEEYEPYQALISLLRGRGWIIPNPLKATDGSDEKELRVVFRSEMKLDLAQ
LLVLDISLITKLHISYKVKCHHIELASEQTPEKRSFYIEMLLALASPODDIPTDE
IEKNKILKETTNRGTC"
7746..8846
/note="YM9920.05, unknown, len: 366, CAI: 0.11, similar to
YK36_YEAST P36156, YK076W, hypothetical protein in Sis2,
62.6% identity in 369 aa overlap"
/codon_start=1
/product="unknown"
/protein_id="CAA88578.1"
/db_xref="GI:732929"
/db_xref="SGD:S0004863"
/db_xref="UniProt/Swiss-Prot:Q04806"
/translation="MSEKASNNKAEPKQSPFREIISADHPITYKPAKGYWLYVAL
PCWPAQRTLTALKGAPITIGCSVAHMLDDKGRFLEEGDGTNERHWFDIAGGIS
SNLNTSTPANI PNNAHRLLDVGTDEPHYKRLSDYFKPTKDYKGRFTVPVLDL
ETCTIVNNESSDIIGMNSAAFDFEVEGEEVROVLRPSLEAOITENSVMYDKING
VYKGAECACVVERVTSLSFOYLDKLENLLDKYITLDEBYGKNKKDKILDYRPAIG
VTTEADRLVLPITVRPVDVYVHGFKNCLATIRDDYSRIHTWLKNIYWRHEAFORTTD
FTHIKGYTRSQPRVPDITPLGPKPDIRPP"
complement (10146..10550)
/note="YM9920.06c, unknown, len: 134, CAI: 0.13"
/codon_start=1
/product="unknown"
/protein_id="CAA88579.1"
/db_xref="GI:732930"
/db_xref="SGD:S0004865"
/db_xref="UniProt/Swiss-Prot:Q04814"
/translation="MECKVFSYVIRTRIGFKPLSTIYTPVSSSLSFDEKACFPFKW
HELNMQKQEFIQRFVKNYRHOYPSKTNVSLKLSIGMDEHNDSPSVFGIFYNDIWK
SFKNQEGTNNDNKSGRSFHSFQKLLIQK"
complement (10777..12021)
/note="YM9920.07c, unknown, len: 414, CAI: 0.13,
hydrophobic domains"
/codon_start=1
/product="unknown"
/protein_id="CAA88580.1"
/db_xref="GI:732931"
/db_xref="GOA:Q04835"
/db_xref="SGD:S0004866"
/db_xref="UniProt/Swiss-Prot:Q04835"
/translation="MMPSPVKMKRNNTHLLSVKNNNTSLQLPSTTRSLSPKESNS
NEDFNVQDNETTLQRIKSKYKPNIGLVLTIVSYFFNSAMVSVTKLENDDDIANDR
QIKPLQALLVRLVITGLIYIYINKSTISDVFGKPEVRKWLVRGKGFQFVGM
YYSMLVITSDAVLITPLAPSLFISLWILRERFTKALGSLISLLGVLIYRPSF
LPTGPELTDSSQIVSSDPKSLIATLVGLWGLVMSCVYIIRYIKRAHAIMSVS
YFSLITAVISFIGINTIPSMKQFIPHSKQWILFGLVSGFIFQLLLTGIIQERAG

```

CDS

```

7746..8846
/note="YM9920.05, unknown, len: 366, CAI: 0.11, similar to
YK36_YEAST P36156, YK076W, hypothetical protein in Sis2,
62.6% identity in 369 aa overlap"
/codon_start=1
/product="unknown"
/protein_id="CAA88578.1"
/db_xref="GI:732929"
/db_xref="SGD:S0004863"
/db_xref="UniProt/Swiss-Prot:Q04806"
/translation="MSEKASNNKAEPKQSPFREIISADHPITYKPAKGYWLYVAL
PCWPAQRTLTALKGAPITIGCSVAHMLDDKGRFLEEGDGTNERHWFDIAGGIS
SNLNTSTPANI PNNAHRLLDVGTDEPHYKRLSDYFKPTKDYKGRFTVPVLDL
ETCTIVNNESSDIIGMNSAAFDFEVEGEEVROVLRPSLEAOITENSVMYDKING
VYKGAECACVVERVTSLSFOYLDKLENLLDKYITLDEBYGKNKKDKILDYRPAIG
VTTEADRLVLPITVRPVDVYVHGFKNCLATIRDDYSRIHTWLKNIYWRHEAFORTTD
FTHIKGYTRSQPRVPDITPLGPKPDIRPP"
complement (10146..10550)
/note="YM9920.06c, unknown, len: 134, CAI: 0.13"
/codon_start=1
/product="unknown"
/protein_id="CAA88579.1"
/db_xref="GI:732930"
/db_xref="SGD:S0004865"
/db_xref="UniProt/Swiss-Prot:Q04814"
/translation="MECKVFSYVIRTRIGFKPLSTIYTPVSSSLSFDEKACFPFKW
HELNMQKQEFIQRFVKNYRHOYPSKTNVSLKLSIGMDEHNDSPSVFGIFYNDIWK
SFKNQEGTNNDNKSGRSFHSFQKLLIQK"
complement (10777..12021)
/note="YM9920.07c, unknown, len: 414, CAI: 0.13,
hydrophobic domains"
/codon_start=1
/product="unknown"
/protein_id="CAA88580.1"
/db_xref="GI:732931"
/db_xref="GOA:Q04835"
/db_xref="SGD:S0004866"
/db_xref="UniProt/Swiss-Prot:Q04835"
/translation="MMPSPVKMKRNNTHLLSVKNNNTSLQLPSTTRSLSPKESNS
NEDFNVQDNETTLQRIKSKYKPNIGLVLTIVSYFFNSAMVSVTKLENDDDIANDR
QIKPLQALLVRLVITGLIYIYINKSTISDVFGKPEVRKWLVRGKGFQFVGM
YYSMLVITSDAVLITPLAPSLFISLWILRERFTKALGSLISLLGVLIYRPSF
LPTGPELTDSSQIVSSDPKSLIATLVGLWGLVMSCVYIIRYIKRAHAIMSVS
YFSLITAVISFIGINTIPSMKQFIPHSKQWILFGLVSGFIFQLLLTGIIQERAG

```

CDS

```

complement (10146..10550)
/note="YM9920.06c, unknown, len: 134, CAI: 0.13"
/codon_start=1
/product="unknown"
/protein_id="CAA88579.1"
/db_xref="GI:732930"
/db_xref="SGD:S0004865"
/db_xref="UniProt/Swiss-Prot:Q04814"
/translation="MECKVFSYVIRTRIGFKPLSTIYTPVSSSLSFDEKACFPFKW
HELNMQKQEFIQRFVKNYRHOYPSKTNVSLKLSIGMDEHNDSPSVFGIFYNDIWK
SFKNQEGTNNDNKSGRSFHSFQKLLIQK"
complement (10777..12021)
/note="YM9920.07c, unknown, len: 414, CAI: 0.13,
hydrophobic domains"
/codon_start=1
/product="unknown"
/protein_id="CAA88580.1"
/db_xref="GI:732931"
/db_xref="GOA:Q04835"
/db_xref="SGD:S0004866"
/db_xref="UniProt/Swiss-Prot:Q04835"
/translation="MMPSPVKMKRNNTHLLSVKNNNTSLQLPSTTRSLSPKESNS
NEDFNVQDNETTLQRIKSKYKPNIGLVLTIVSYFFNSAMVSVTKLENDDDIANDR
QIKPLQALLVRLVITGLIYIYINKSTISDVFGKPEVRKWLVRGKGFQFVGM
YYSMLVITSDAVLITPLAPSLFISLWILRERFTKALGSLISLLGVLIYRPSF
LPTGPELTDSSQIVSSDPKSLIATLVGLWGLVMSCVYIIRYIKRAHAIMSVS
YFSLITAVISFIGINTIPSMKQFIPHSKQWILFGLVSGFIFQLLLTGIIQERAG

```

CDS

```

complement (10777..12021)
/note="YM9920.07c, unknown, len: 414, CAI: 0.13,
hydrophobic domains"
/codon_start=1
/product="unknown"
/protein_id="CAA88580.1"
/db_xref="GI:732931"
/db_xref="GOA:Q04835"
/db_xref="SGD:S0004866"
/db_xref="UniProt/Swiss-Prot:Q04835"
/translation="MMPSPVKMKRNNTHLLSVKNNNTSLQLPSTTRSLSPKESNS
NEDFNVQDNETTLQRIKSKYKPNIGLVLTIVSYFFNSAMVSVTKLENDDDIANDR
QIKPLQALLVRLVITGLIYIYINKSTISDVFGKPEVRKWLVRGKGFQFVGM
YYSMLVITSDAVLITPLAPSLFISLWILRERFTKALGSLISLLGVLIYRPSF
LPTGPELTDSSQIVSSDPKSLIATLVGLWGLVMSCVYIIRYIKRAHAIMSVS
YFSLITAVISFIGINTIPSMKQFIPHSKQWILFGLVSGFIFQLLLTGIIQERAG

```

misc_feature

```

complement (4197..4199)
/note="possible splice acceptor sequence, cag"

```

RGSLMYTQLLYAVFWDVALYKEWPNIMWSWIGMIIISATLWVIRAIRAANNETTAKDL
 TPIIDDEENSIPLETDFLSDSK
 complement (12446..12754)
 /notes="YM9920.08c, unknown, len: 103, CAI: 0.07,
 questionable orf"
 /codon_start=1
 /product="unknown"
 /protein_id="CAA88581.1"
 /db_xref="GI:732932"
 /db_xref="GOA:Q04838"
 /db_xref="SGD:S0004867"
 /db_xref="UniProt/Swiss-Prot:Q04838"
 /translation="MWPLILLLFLSKFSLFRPNVHVLTKYTAIVNTKWQTPSII
 DVTYTHVFTMTIILVLRKOMQSIHAFGLSLCLPSHVLDFSIIVRDLISWYFLETAV
 "

12832..13398
 /notes="YM9920.09, unknown, len: 188, CAI: 0.15,
 coiled-coil domain"
 /codon_start=1
 /product="unknown"
 /protein_id="CAA88582.1"
 /db_xref="GI:732933"
 /db_xref="GOA:Q04839"
 /db_xref="SGD:S0004868"
 /db_xref="UniProt/Swiss-Prot:Q04839"
 /translation="MPLSIWADAPDEEPIKKQPKHRSNNNNKNNNRWNSNSSN
 NKKDSVYKNNKHESKTKNKIKETLPREKKPHSOKKISPVSESLAINPFSOKA
 TEISPPVSPSKMTTKTOSKODTASMKMLKKKIEQREILKTHHKQOQVLMDF
 LNDEGSSNWDDDEEELLQRLATSLKI"
 complement (13776..13958)

gene

Query Match 99.6%; Score 720.4; DB 8; Length 23498;
 Best Local Similarity 99.9%; Pred. No. 4.2e-206;
 Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTTCGATTAGCAGCACACATACATAGCTGCGTCATAAAATACACTACGAAAA 60
 DB 8860 CTTTCGATTAGCAGCACACATACATAGCTGCGTCATAAAATACACTACGAAAA 8919

QY 61 ACCATAAGACAAAGCGATACCTACTTGAAGGAAAGGACGCGTCTGAAGGGGAT 120
 DB 8920 ACCATAAGACAAAGCGATACCTACTTGAAGGAAAGGACGCGTCTGAAGGGGAT 8979

QY 121 GGGGGCTAAGAGTCATCTCTTTTCCCTTCGGGTCGGGACCCGGGACCCCTCCT 180
 DB 8980 GGGGGCTAAGAGTCATCTCTTTTCCCTTCGGGTCGGGACCCGGGACCCCTCCT 9039

QY 181 CTCGGCGCAGATTTCTCTTTTCATATCTCTTTTATTTCTATCTCCGTTGAAGCAAC 240
 DB 9040 CTCGGCGCAGATTTCTCTTTTCATATCTCTTTTATTTCTATCTCCGTTGAAGCAAC 9099

QY 241 GCACTATGACTAATGGTGTGGACATCTCCATGGCTGTGACTTGTGTATCTCAGT 300
 DB 9100 GCACTATGACTAATGGTGTGGACATCTCCATGGCTGTGACTTGTGTATCTCAGT 9159

QY 301 GGTAAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAAATCTAGAAACGGGGCTACA 360
 DB 9160 GGTAAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAAATCTAGAAACGGGGCTACA 9219

QY 361 GTCTCGAATAGNATAATAGGCGATTTTGTAGCGCGCGCGCGCGCGCGCTTTCCCA 420
 DB 9220 GTCTCGAATAGNATAATAGGCGATTTTGTAGCGCGCGCGCGCGCGCGCTTTCCCA 9279

QY 421 ATAGGAGGCGCAGTTTATCGGCGAGCTCTACTTCTTCTATTTGGGTAAAGCCCTTTC 480
 DB 9280 ATAGGAGGCGCAGTTTATCGGCGAGCTCTACTTCTTCTATTTGGGTAAAGCCCTTTC 9339

QY 481 TGTTCGCGCAGTGGTGTGCGAGGCTGCGCGGAGACATAGTGATAGGAGTGTAC 540
 DB 9340 TGTTCGCGCAGTGGTGTGCGAGGCTGCGCGGAGACATAGTGATAGGAGTGTAC 9399

QY 541 TTTTCGATGAGAGATTAAGCAAGCGGAAAAAATATAGCTAGCTGGAGTGTGTTTCAA 600

DB 9400 TTTTCGATGAGAGATTAAGCAAGCGGAAAAAATATAGCTAGCTGGAGTGTGTTTCAA 9459

QY 601 TCATATAAAGGAGCAAAATTTGCTCCTACTATGTGACAGTTTCTGGAGCTCTTAACCTT 660
 DB 9460 TCATATAAAGGAGCAAAATTTGCTCCTACTATGTGACAGTTTCTGGAGCTCTTAACCTT 9519

QY 661 TATTGACAGGACTATCAAAATCATACAGATTTGTCAAAAAAAGAAAGACTTAATAATAA 720
 DB 9520 TATTGACAGGACTATCAAAATCATACAGATTTGTCAAAAAAAGAAAGACTTAATAATAA 9579

QY 721 CA 722

DB 9580 AA 9581

RESULT 6
 AX536716
 LOCUS AX536716 680 bp DNA linear PAT 22-NOV-2002
 DEFINITION Sequence 317 from Patent WO02064766.
 ACCESSION AX536716
 VERSION AX536716.1 GI:25263152
 KEYWORDS
 SOURCE Saccharomyces cerevisiae (baker's yeast)
 ORGANISM Saccharomyces cerevisiae
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 1
 CONTRERAS, R.H., Eberhardt, I., Luyten, W.H. and Reekmans, R.J.
 Bax-responsive genes for drug target identification in yeast and
 fungi
 Patent: WO 02064766-A 317 22-AUG-2002;
 JANSSEN PHARMACEUTICA N.V. (BE)
 Location/Qualifiers
 1..680
 /organism="Saccharomyces cerevisiae"
 /mol_type="unassigned DNA"
 /db_xref="taxon:4932"

ORIGIN

Query Match 68.8%; Score 497.4; DB 6; Length 680;
 Best Local Similarity 99.8%; Pred. No. 6.7e-139;
 Matches 498; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 224 ATCCCGTTGAAGCAACCGCCTATGCTAAATGGTGGACATCTCCATGGCTGTGACT 283
 DB 1 ATCCCGTTGAAGCAACCGCCTATGCTAAATGGTGGACATCTCCATGGCTGTGACT 60

QY 284 TGTGTATCTCAGTGGTAAACCGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAAAT 343
 DB 61 TGTGTATCTCAGTGGTAAACCGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAAAT 120

QY 344 CTAGAACGGGCTACAGTCTCGATAATAGATAATAGCGCATTTTGTAGCGCGGCC 403
 DB 121 CTAGAACGGGCTACAGTCTCGATAATAGATAATAGCGCATTTTGTAGCGCGGCC 180

QY 404 GCGGCGCCGCTTCCCAATAGGAGCGCGAGTTTATCGCGGAGCTCTACTTCTTCCTAT 463
 DB 181 GCGGCGCCGCTTCCCAATAGGAGCGCGAGTTTATCGCGGAGCTCTACTTCTTCCTAT 240

QY 464 TTGGGTAAAGCCCTTTCTGTTTTCGGCCAGTGGTGTGCTGACGGCTGCGCGGAGACATA 523
 DB 241 TTGGGTAAAGCCCTTTCTGTTTTCGGCCAGTGGTGTGCTGACGGCTGCGCGGAGACATA 300

QY 524 GTGATAAGGATGTAACTTTTCGATGAGAGATTAGCAAGCGGAAAAAATATGCTAGC 583
 DB 301 GTGATAAGGATGTAACTTTTCGATGAGAGATTAGCAAGCGGAAAAAATATGCTAGC 360

QY 584 TGGGAGTGTGTTTTCATATAAAGGAGAAATTTGTGCTCACTATGTGACAGTTTC 643
 DB 361 TGGGAGTGTGTTTTCATATAAAGGAGAAATTTGTGCTCACTATGTGACAGTTTC 420

QY 644 TGGGAGCTTTAACTTTTATTTGACAGGACTATCAATCATACAGATTTGTCAAAAAA 703